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Attorney Docket No. 979-1-017

B2 (Amended) Fig. 9A-9B illustrate a comparison of the conceptual amino acid sequences for GRO-1 (SEQ ID NO:2) and hgro-1p as deduced from SEQ ID NO:3;

Please amend the paragraph on Page 14, lines 1-28 as follows:

B3 (Amended) Database searches also identified a homologous human expressed sequence tag (Genbank ID: Z40724). The human clone has been used to derive a sequence tagged site (STS). This means that the genetic and physical position of the human *gro-1* homologue is known. It maps to chromosome 1, 122.8 cR from the top of Chr 1 linkage group and between the markers D1S255 and D1S2861. This information was found in the UniGene database or the National Center for Biotechnology Information (NCBI). We have sequenced Z40724 by classical methods but found that Z40724 is not a full length cDNA clone as it does not contain an initiator methionine nor the poly A tail. We used the sequence of Z40724 to identify further clones by database searches. We found one clone (Genbank ID: AA332152) which extended the sequence 5' by 28 nucleotides, as well as one clone (Genebank ID: AA121465) which extended the sequence substantially in the 3' direction but didn't include the poly A tail. We then used AA121465 to identify an additional clone (AA847885) extending the sequence to the poly A tail. Fig. 8 shows the full sequence with the putative initiator ATG shown in bold and the sequence of Z60724 is shown underlined. A comparison of the conceptual amino acid sequences for GRO-1 (SEQ ID NO:2) and hgro-1p as deduced from SEQ ID NO:3, is shown in Fig. 9. Amino acid identities are indicated by a dot. Both sequences contain a region with a zinc finger motif which is shown underlined.

IN THE CLAIMS:

Please cancel claims 2-6 without prejudice or disclaimer.